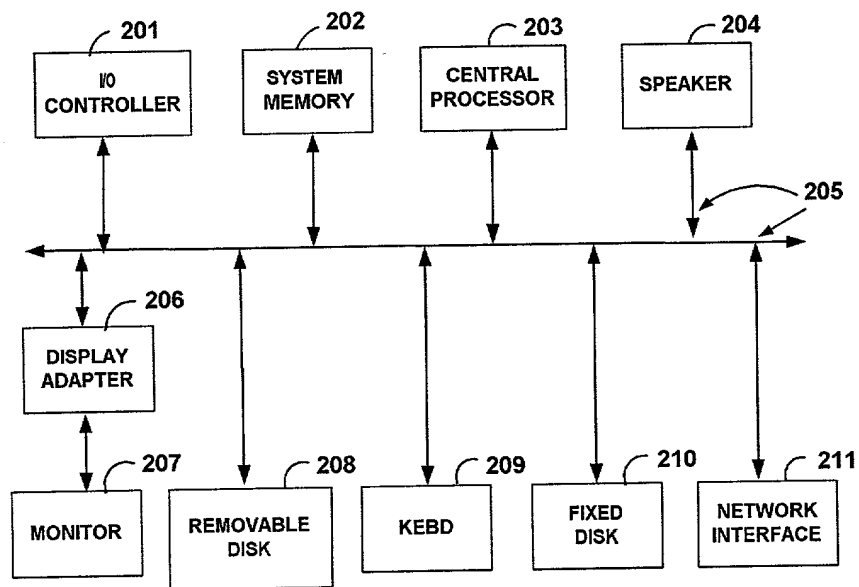


**Figure 1**



**Figure 2**

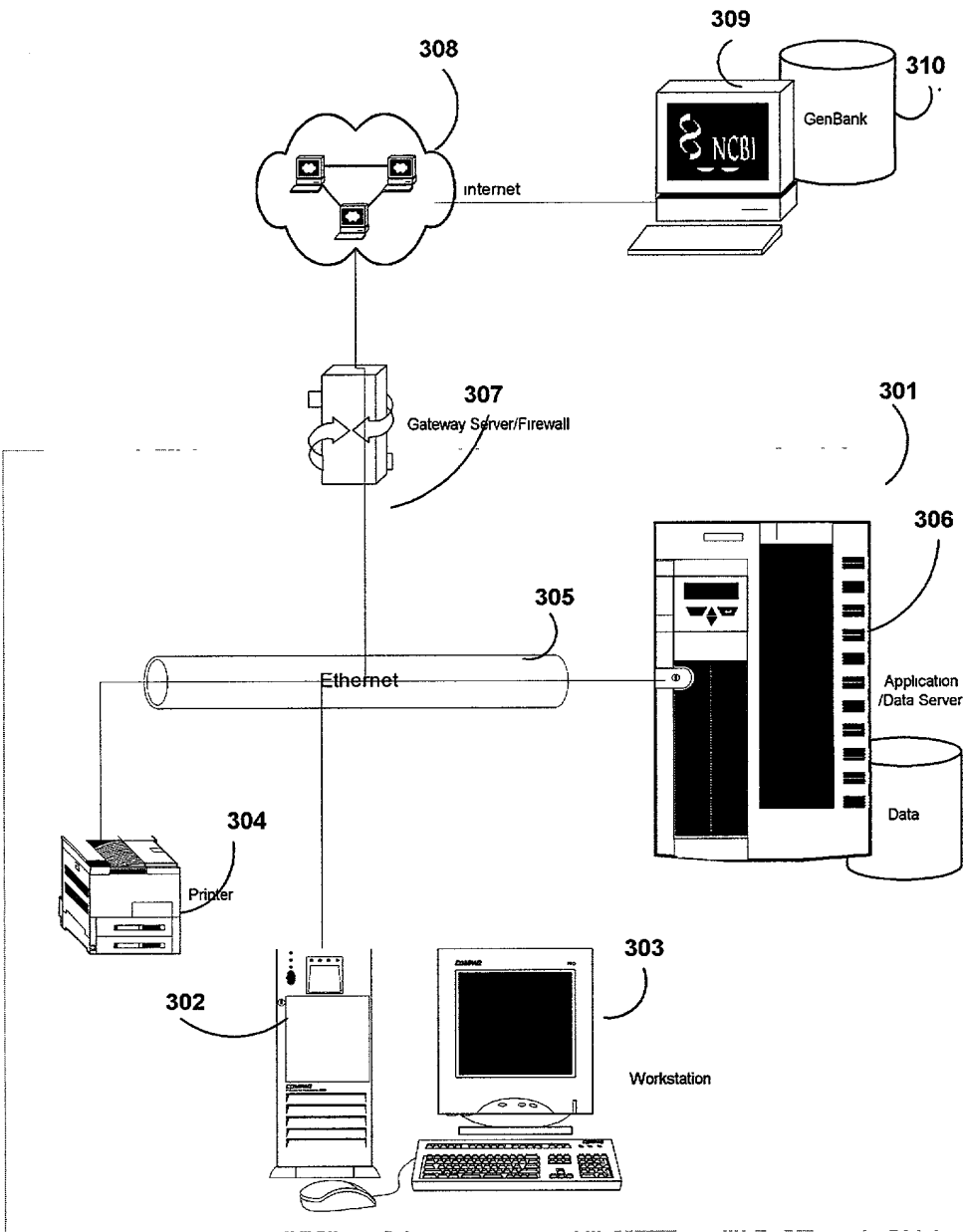


FIGURE 3

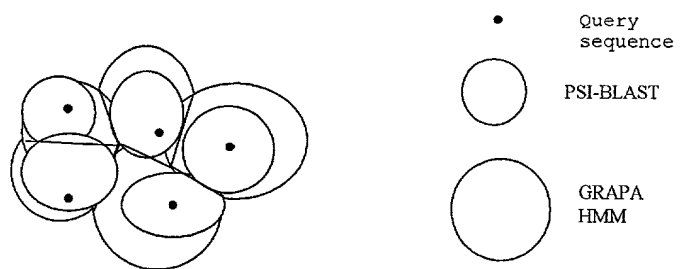
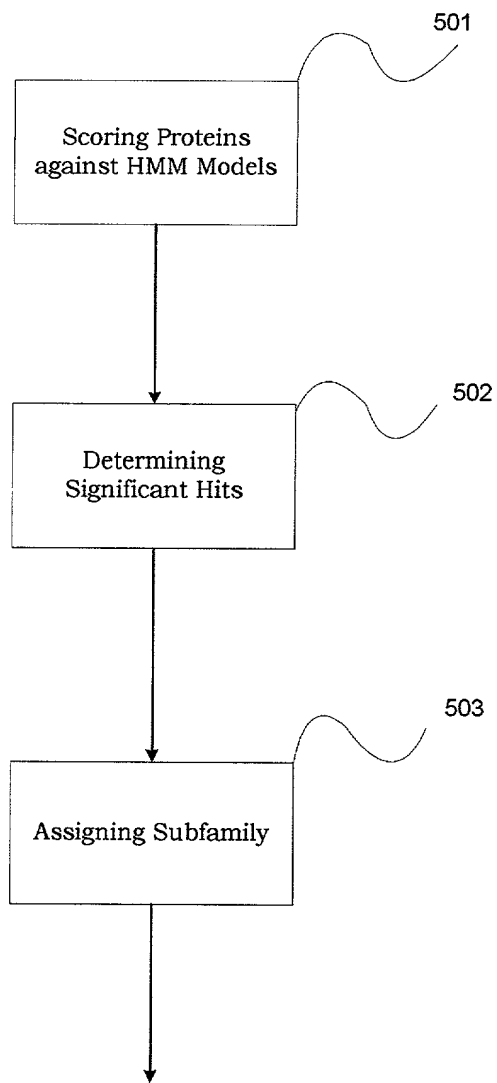
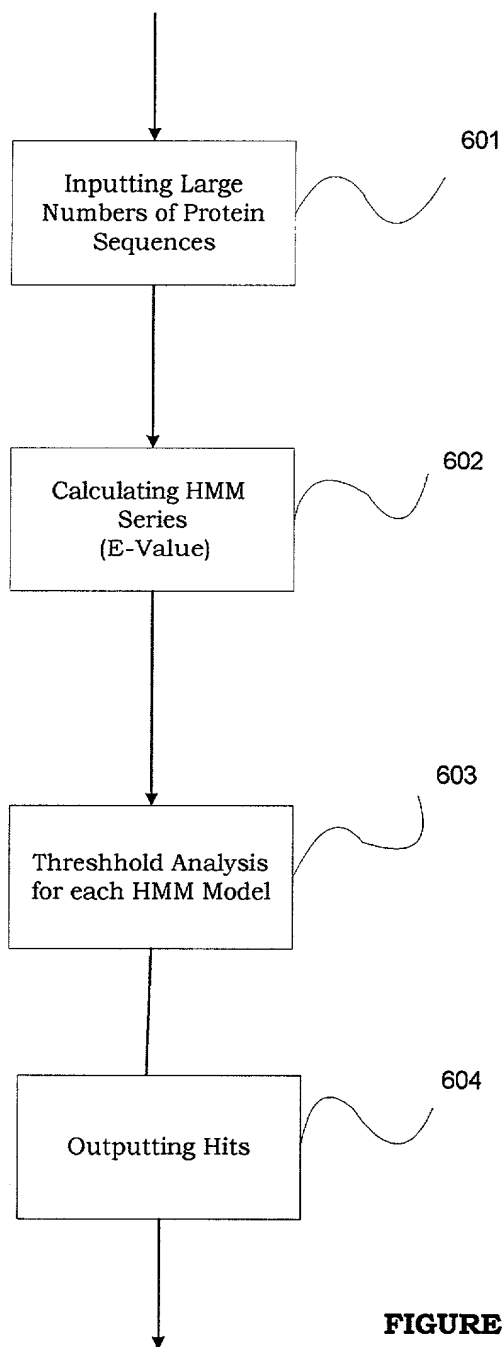


FIGURE 4



**FIGURE 5**



**FIGURE 6**

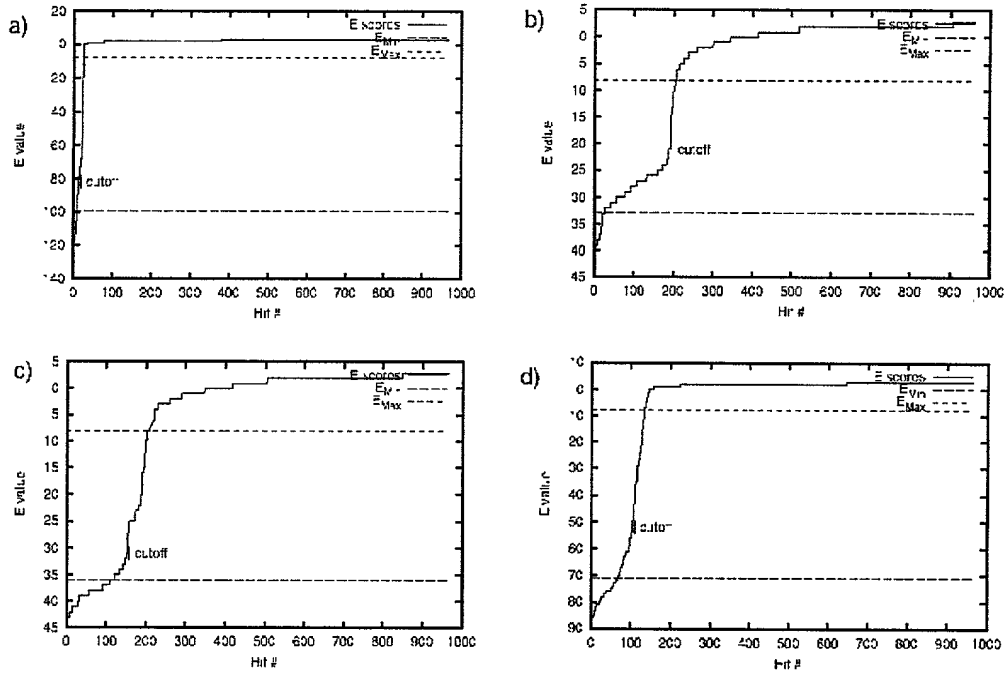
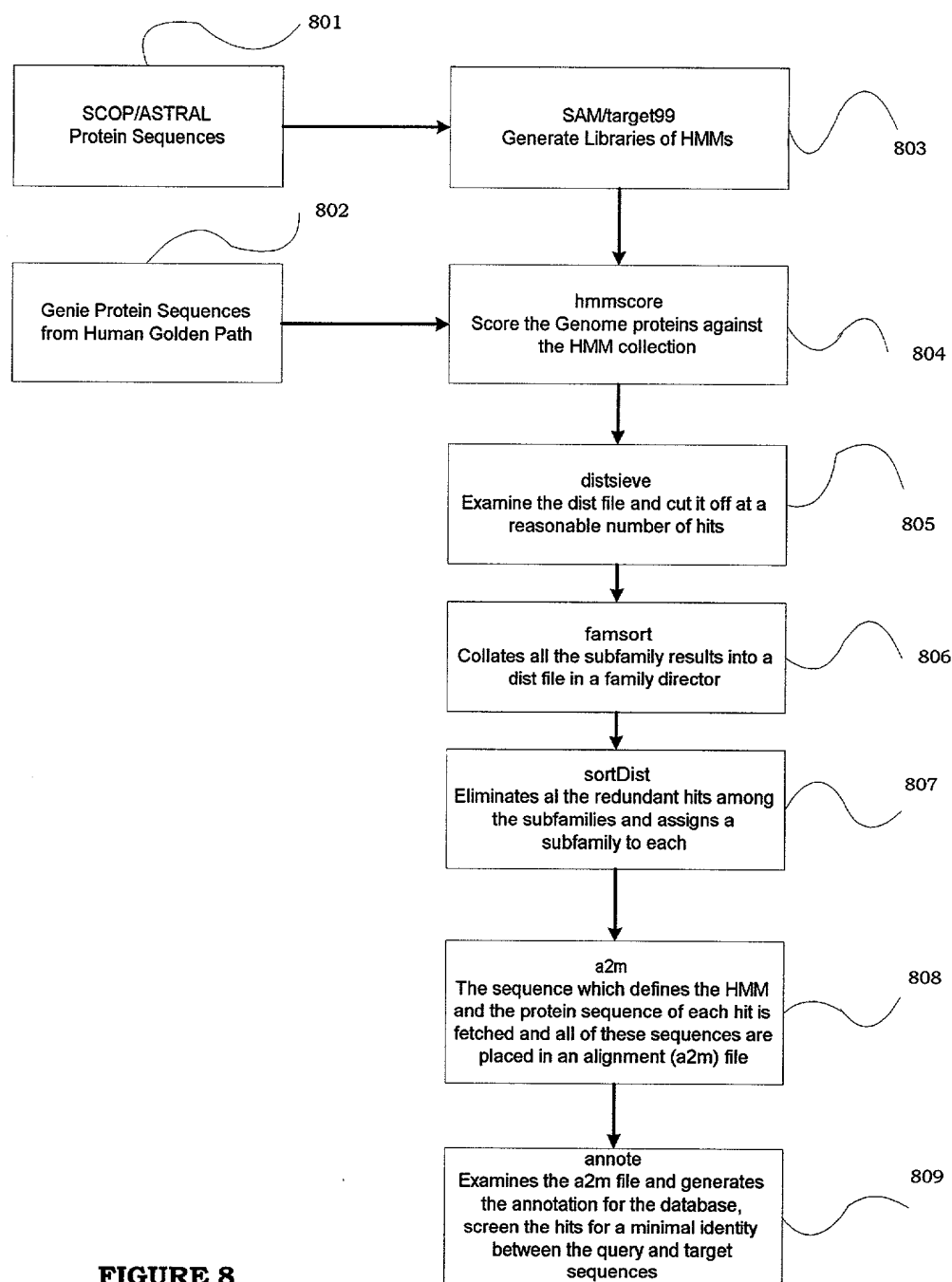


FIGURE 7



**FIGURE 8**



Alignment 1:

```

1>GRAPAHIT1 1 LLQDSLLRLKDYRQCFCSDVALNEAVQQMVNSGEAAAKEEWVATVTQLL
2>lvhr 1 SVQDLNLDLLSDGSGCYSLPSQPCNE VTPRIYVGNASVAQD IPKLQKL

1>GRAPAHIT1 51 MGIEQALSADSSGSILKVSSSTTGLVRLTNNLIQVIDCSMAVQEEAKEPH
2>lvhr 51 GITHVLNAAEGRSFMHVNTNAN

1>GRAPAHIT1 101 VSSVLPWIIHRIIWQEEEDTFHSLCHQQQLQNPAAEGMSETPMLPSSMLL
2>lvhr 101 FYK DSGIT

1>GRAPAHIT1 151 LNTAHEYLGRRSWCCNSDGA LLRFYVRVLQKELAASTSEDTHPYKEELET
2>lvhr 151 YLGIKA NDTQEFN

1>GRAPAHIT1 201 ALEQCFYCLYSFSPKSKKARYLEEHSQQVDLIWEDALFMFEYFKPKTLP
2>lvhr 201 LSAYFERAA

1>GRAPAHIT1 251 EFDSYKTSTVSADLANLLKRIATIVRTERPALSLDKVSAYIEGTSTVEP
2>lvhr 251 DF IDQALAQKNGRVL VH

1>GRAPAHIT1 301 CLPEGADPSPPVVNELYLLADYHFKNKEQSKAIKFYMHDICICPNREDS
2>lvhr 301 C REGYSRSPTLV IAYLMMR QKMDVKSALSIVRQNRIGPN DG

1>GRAPAHIT1 351 WAGMALARASRIQDKLNSNE LKS
2>lvhr 351 F LAQLCQLNDR LAKEGKLKP

```

Alignment 2:

```

1a17 PPADGALKRAEELKTQAN-----DYFKAKDYENAIKFYSQAIE
GRAPAHIT2 PLCKQALEDELEKTS GHDHPDVATMLNIALVYRDQNKYKEAAHLLNDALA
GRAPAHIT3 KDWK GALDAFSAVQD PHSRICFN----IGCMYTILKNMTEAEKAFTR SIN

1a17 L-----NPSNAIYYGNRSLAYLRTECYGYALGDATR-AIELDKKYIK
GRAPAHIT2 IREKTLGKDHPAVAATLNNLAVLYGKRGKYKEAEPLCKR-ALEIREKVLG
GRAPAHIT3 R-----DKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLI

1a17 GYYRRAASNMA-----LG-----KFRAALRDYET-----
GRAPAHIT2 KFHPDVAKQLSNLALLCQNGKAEVEYYYRRALEIYATRL---GPDDP
GRAPAHIT3 DYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHS

1a17 -VVKVKP-----HDKDAKMKYQECNKIVKQKAF-----
GRAPAHIT2 NVAKTKNNLASCYLKQGYQDAETLYKEILTRAHEKEFGSVNGDNKPIWM
GRAPAHIT3 KIDKAMECVWKQKLYEPVVI PVGKLF RPNERQVAQLAKKDYL GKATVVAS

1a17 ---ERAIA-----GDEHKR-----SVVDSLDIESMTIEDEYS
GRAPAHIT2 HAEEREES-----KDKRRDSAPYGEYGSWYKACKVDSPVTNTLR
GRAPAHIT3 VVDQDSFSGFAPLQPQAAEPPPRPKTPEIFRALEGEAHRVLFGEV

```

FIGURE 9

0.1

FIGURE 10

FIGURE 10